

Run on: August 19, 2003, 09:30:59 ; Search time 4316 Seconds
(without alignments)
12805.463 Million cell updates/sec

ON nucleic - nucleic search, using sw model

Title: US-09-494-297-1

Perfect score: 2274

Sequence: 1 atgaaaaaaacaagtttcc.....ggataagaaacatgactag 2274

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: em_leetba:*

2: em_lesthum:*

3: em_lestin:*

4: em_leetu:*

5: em_lestov:*

6: em_lestapl:*

7: em_leetro:*

8: em_htcc:*

9: qb_est1:*

10: qb_est2:*

11: qb_htcc:*

12: qb_est3:*

13: qb_est4:*

14: qb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mut:*

24: em_gss_pro:*

25: em_gss_rid:*

26: em_gss_pig:*

27: em_gss_vrl:*

28: qb_gss1:*

29: qb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
C 1	70.2	3.1	1101	29 CNS0039G	AL063921 Drosophila melanogaster genome survey sequence TEP3 end of BAC #
C 2	69.4	3.1	1200	13 BX43758	BX43758 BX43758
C 3	66.8	2.9	1201	13 BX462660	BX462660 BX462660
C 4	65.2	2.9	960	13 BX346155	BX346155 BX346155

RESULTS

RESULT 1

LOCUS CNS0039G/C

DEFINITION Drosophila melanogaster genome survey sequence TEP3 end of BAC #

VERSION AL063921.1 GI:4941778

KEYWORDS GSS.

ORGANISM Drosophila melanogaster (fruit fly)

SOURCE Bacteria; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidea; Drosophilidae; Drosophila; (bases 1 to 101)

REFERENCE Genoscope.

AUTHORS Direct Submission

TITLE Submitted (07-JUN-1999) Genoscope - centre National de Sequencage : BP 191 91006 EVRY cedex 1-FRANCE (E-mail : seqref@genoscope.cns.fr)

COMMENT

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamsoor in Pieter de Jong's laboratory in the Department of

GenCore version 5.1.6

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AL1536104 AL1536104

BM169292 EST571815

BX41058 BX41058

BX448176 BX448176

BX449176 BX449176

BX166601 EST569124

BX341255 BX341255

BX439779 BX439779

BX377526 BX377526

BX376097 BX376097

BX436885 BX436885

BX415231 BX415231

BX163047 EST1565570

BX169947 EST572470

AL09706 Drosophila

AL10396 Drosophili

AL10595 Drosophili

AL146885 BX436885

AL06943 Drosophili

BX380865 BX380865

AZ697380 ENT10525

AL173696 Tetradon

AL101595 Drosophili

AL147405 Anophales

AL419462 T3 end of

AL16578 Drosophili

BM160720 EST56243

AL1514901 AL1514901

AL1514901 AL1514901

BJ446581 BJ446581

A2683582 ENIKK471R

AL244551 Tetradon

AL053632 Drosophili

AL151421 AL151421

AL1536104 AL1536104

BX436282 BX436282

BX415878 BX415878

BX446296 BX446296

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of *Drosophila* DNA provided by the BGP from the isogenic strain y2; cn bw SP, the same strain used for the BGP's PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at <http://bacpac.med.buffalo.edu/drosophila.bac.htm>.

FEATURES	source	ORGANISM	LOCUS	DEFINITION	5' PRIME	ACCESSION	VERSION	KEYWORDS	SOURCE
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		/clone.lib="RPCI-98"	VERSION	BX437758.1					
			EST						
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			REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
			AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.					
			TITLE	Full-length cDNA libraries and normalization					
			JOURNAL	Unpublished					
			COMMENT	Contact: Genoscope					
				Genoscope - Centre National de Séquençage					
				BP 191 91006 EVRY cedex - France					
				Email: seqref@genoscope.cns.fr					
				Library was constructed by Life Technologies, a division of Invitrogen. Contact: Feng Liang Email: liang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Parady					
				Paradigm Avenue Genoscope Sequence ID: CS0CAP008CA01QPI					
FEATURES	source	ORGANISM	LOCUS	DEFINITION	5' PRIME	ACCESSION	VERSION	KEYWORDS	SOURCE
BASE COUNT	515 a 30 c 71 g 310 t 274 others	1. .1200	BX437758	1200 bp mRNA	linear	EST	15-MAY-2003		
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			AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.					
			TITLE	Full-length cDNA libraries and normalization					
			JOURNAL	Unpublished					
			COMMENT	Contact: Genoscope					
				Genoscope - Centre National de Séquençage					
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				Library was constructed by Life Technologies, a division of Invitrogen. Contact: Feng Liang Email: liang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Parady					
				Paradigm Avenue Genoscope Sequence ID: CS0CAP008CA01QPI					
FEATURES	source	ORGANISM	LOCUS	DEFINITION	5' PRIME	ACCESSION	VERSION	KEYWORDS	SOURCE
BASE COUNT	515 a 30 c 71 g 310 t 274 others	1. .1200	BX437758	1200 bp mRNA	linear	EST	15-MAY-2003		
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		/mol_type="mRNA"	DEFINITION	BX437758	Homo sapiens	mRNA sequence.			
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			REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
			AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.					
			TITLE	Full-length cDNA libraries and normalization					
			JOURNAL	Unpublished					
			COMMENT	Contact: Genoscope					
				Genoscope - Centre National de Séquençage					
				BP 191 91006 EVRY cedex - France					
				Email: seqref@genoscope.cns.fr					
				Library was constructed by Life Technologies, a division of Invitrogen. Contact: Feng Liang Email: liang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Parady					
				Paradigm Avenue Genoscope Sequence ID: CS0CAP008CA01QPI					
FEATURES	source	ORGANISM	LOCUS	DEFINITION	5' PRIME	ACCESSION	VERSION	KEYWORDS	SOURCE
BASE COUNT	515 a 30 c 71 g 310 t 274 others	1. .1200	BX437758	1200 bp mRNA	linear	EST	15-MAY-2003		
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		/mol_type="mRNA"	DEFINITION	BX437758	Homo sapiens	mRNA sequence.			
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		/clone="CS0CAP008YB01"	ACCESSION	BX437758					
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			REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
			AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.					
			TITLE	Full-length cDNA libraries and normalization					
			JOURNAL	Unpublished					
			COMMENT	Contact: Genoscope					
				Genoscope - Centre National de Séquençage					
				BP 191 91006 EVRY cedex - France					
				Email: seqref@genoscope.cns.fr					
				Library was constructed by Life Technologies, a division of Invitrogen. Contact: Feng Liang Email: liang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Parady					
				Paradigm Avenue Genoscope Sequence ID: CS0CAP008CA01QPI					
FEATURES	source	ORGANISM	LOCUS	DEFINITION	5' PRIME	ACCESSION	VERSION	KEYWORDS	SOURCE
BASE COUNT	515 a 30 c 71 g 310 t 274 others	1. .1200	BX437758	1200 bp mRNA	linear	EST	15-MAY-2003		
ORIGIN		/organism="Homo sapiens"	LOCUS	BX437758	Homo sapiens	THYMUS	Homo sapiens	cDNA clone	CS0CAP008YB01
		/mol_type="mRNA"	DEFINITION	BX437758	Homo sapiens	mRNA sequence.			
		/db_xref="taxon:9606"	5' PRIME						
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		/clone.lib="Homo sapiens THYMUS"	VERSION	BX437758.1					
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			REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
			AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.					
			TITLE	Full-length cDNA libraries and normalization					
			JOURNAL	Unpublished					
			COMMENT	Contact: Genoscope					
				Genoscope - Centre National de Séquençage					
				BP 191 91006 EVRY cedex - France					
				Email: seqref@genoscope.cns.fr					
				Library was constructed by Life Technologies, a division of Invitrogen. Contact: Feng Liang Email: liang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Parady					
				Paradigm Avenue Genoscope Sequence ID: CS0CAP008CA01QPI					
FEATURES	source	ORGANISM	LOCUS	DEFINITION	5' PRIME	ACCESSION	VERSION	KEYWORDS	SOURCE
BASE COUNT	515 a 30 c 71 g 310 t 274 others	1. .1200	BX437758	1200 bp mRNA	linear	EST	15-MAY-2003		
ORIGIN		/organism="Homo sapiens"	LOCUS	BX437758	Homo sapiens	THYMUS	Homo sapiens	cDNA clone	CS0CAP008YB01
		/mol_type="mRNA"	DEFINITION	BX437758	Homo sapiens	mRNA sequence.			
		/db_xref="taxon:9606"	5' PRIME						
		/clone="CS0CAP008YB01"	ACCESSION	BX437758					
		/clone.lib="Homo sapiens THYMUS"	VERSION	BX437758.1					
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			REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
			AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.					
			TITLE	Full-length cDNA libraries and normalization					
			JOURNAL	Unpublished					
			COMMENT	Contact: Genoscope					
				Genoscope - Centre National de Séquençage					
				BP 191 91006 EVRY cedex - France					
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				Library was constructed by Life Technologies, a division of Invitrogen. Contact: Feng Liang Email: liang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Parady					
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FEATURES	source	ORGANISM	LOCUS	DEFINITION	5' PRIME	ACCESSION	VERSION	KEYWORDS	SOURCE
BASE COUNT	515 a 30 c 71 g 310 t 274 others	1. .1200	BX437758	1200 bp mRNA	linear	EST	15-MAY-2003		
ORIGIN		/organism="Homo sapiens"	LOCUS	BX437758	Homo sapiens	THYMUS	Homo sapiens	cDNA clone	CS0CAP008YB01
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			AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.					
			TITLE	Full-length cDNA libraries and normalization					
			JOURNAL	Unpublished					
			COMMENT	Contact: Genoscope					
				Genoscope - Centre National de Séquençage					
				BP 191 91006 EVRY cedex - France					
				Email: seqref@genoscope.cns.fr					
				Library was constructed by Life Technologies, a division of Invitrogen. Contact: Feng Liang Email: liang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Parady					
				Paradigm Avenue Genoscope Sequence ID: CS0CAP008CA01QPI					
FEATURES	source	ORGANISM	LOCUS	DEFINITION	5' PRIME	ACCESSION	VERSION	KEYWORDS	SOURCE
BASE COUNT	515 a 30 c 71 g 310 t 274 others	1. .1200	BX437758	1200 bp mRNA	linear	EST	15-MAY-2003		
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			REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
			AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.					
			TITLE	Full-length cDNA libraries and normalization					
			JOURNAL	Unpublished					
			COMMENT	Contact: Genoscope					
				Genoscope - Centre National de Séquençage					
				BP 191 91006 EVRY cedex - France					
				Email: seqref@genoscope.cns.fr					
				Library was constructed by Life Technologies, a division of Invitrogen. Contact: Feng Liang Email: liang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Parady					
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FEATURES	source	ORGANISM	LOCUS	DEFINITION	5' PRIME	ACCESSION	VERSION	KEYWORDS	SOURCE
BASE COUNT	515 a 30 c 71 g 310 t 274 others	1. .1200	BX437758	1200 bp mRNA	linear	EST	15-MAY-2003		
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Query Match		Best Local Similarity	Score	DB	Length	Matches	Local Similarity	Score	DB	Length	Matches
1784	ATAAAAAGAAGTATACCTGTAATTCATTAACATGAGAAAACGGTACTGGT	37.6%	Score 65.2;	DB 13;	Length 960;	134;	Conservative	54;	Mismatches 168;	Indels 0;	Gaps 0;
932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAATTAAT	37.6%	Score 65.2;	DB 13;	Length 960;	134;	Conservative	54;	Mismatches 168;	Indels 0;	Gaps 0;
1844	TAGCTGGACAGACTAAGATTCCTTGTAAATGAAATAGCTGACTGGT	37.6%	Score 65.2;	DB 13;	Length 960;	134;	Conservative	54;	Mismatches 168;	Indels 0;	Gaps 0;
872	TTWTTWAAAAAAAAATTTWAAACAAATTTWAAACAAATTTWAAAT	37.6%	Score 65.2;	DB 13;	Length 960;	134;	Conservative	54;	Mismatches 168;	Indels 0;	Gaps 0;
1904	AATGTGCTCTCAAACTTTAACAGATAAACAAACCTCGAATTAAGATG	37.6%	Score 65.2;	DB 13;	Length 960;	134;	Conservative	54;	Mismatches 168;	Indels 0;	Gaps 0;
812	AWAWAAWAAWAAWAAWAAWAWTTTTWAAWAAWAAWAAWAAWAAW	37.6%	Score 65.2;	DB 13;	Length 960;	134;	Conservative	54;	Mismatches 168;	Indels 0;	Gaps 0;
1954	CAACCATTAATTAAACATGGGAAAGTTAACCTCAAGCTTACAGAAGTT	37.6%	Score 65.2;	DB 13;	Length 960;	134;	Conservative	54;	Mismatches 168;	Indels 0;	Gaps 0;
752	AAAACAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAW	37.6%	Score 65.2;	DB 13;	Length 960;	134;	Conservative	54;	Mismatches 168;	Indels 0;	Gaps 0;
2024	CTTACCTCTCAAGAACAGATCTGAGGTAAAGTTAAGTTATGCCAGAG	37.6%	Score 65.2;	DB 13;	Length 960;	134;	Conservative	54;	Mismatches 168;	Indels 0;	Gaps 0;
692	ATRAWATTTAWWAAAWAWAWAWAWAWAWAWAWAWAWAWAWAWAWAW	37.6%	Score 65.2;	DB 13;	Length 960;	134;	Conservative	54;	Mismatches 168;	Indels 0;	Gaps 0;
2084	TAGCAAACTCTACAGTTCAAAACAGAAATACAGTGATGAGACATG	37.6%	Score 65.2;	DB 13;	Length 960;	134;	Conservative	54;	Mismatches 168;	Indels 0;	Gaps 0;
632	YTAATATWWTCTTTAAACAAALAMMMMMAMMMMMTTTT	37.6%	Score 65.2;	DB 13;	Length 960;	134;	Conservative	54;	Mismatches 168;	Indels 0;	Gaps 0;
RESULT 5											
1	FOCUS	AL536104	1201 bp	mRNA	linear	EST	31-MAY-2003	QY	1610	ACATGATGATGATGACTTAGCAGTGTCAAATCCTGTAGATAACGTCACAGTAGA	1669
2	DEFINITION	CS0DF022YC18	5'-PRIME	mRNA sequence.				Db	1200	WYHWTATWWTATWATATAYMACPAWWWTATWAATWAWHTWAWATWTA	1141
3	REFERENCE	AL536104	1	(bases 1 to 1201)				QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
4	AUTHORS	Li,W.B., Gruber,C., Jesse,J. and Polayes,D.						Db	1844	TAGCTGGACAGACTAAGATTCCTTGTAAATGAAATAGCTGACTGGT	1843
5	TITLE	Full-length cDNA libraries and normalization						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
6	JOURNAL	Homo sapiens (human)						Db	1844	TAGCTGGACAGACTAAGATTCCTTGTAAATGAAATAGCTGACTGGT	1843
7	SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
8	COMMENT	On Feb 13, 2001 this sequence version replaced gi:12799597.						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
9	CONTACT	Genoscope						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
10	1	Genoscope - Centre National de Séquençage						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
11	2	BP 191 91006 EYRV cedex - France						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
12	3	Email: secref@genoscope.cns.fr, Web : www.genoscope.cns.fr						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
13	4	Library was constructed by Life Technologies, a division of Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DF022BB090P1.						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
14	FEATURES	Location/Qualifiers						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
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16	REFERENCE	/mol_gname="Homo sapiens"						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
17	AUTHORS	/mol_type="mRNA"						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
18	TITLE	/ab_xref="Taxon:9606"						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
19	JOURNAL	/clones="CS0DF022YC18"						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
20	COMMENT	/tissue_type="FETAL BRAIN"						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
21	1	/dev_stage="fetal"						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
22	2	/clone_lip="Homo sapiens FETAL BRAIN"						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
23	3	/note="Organ: brain; Vector: PCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECORV sites of the PCMVSPORT 6 vector. Library was not normalized."						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
24	4	USE COUNT	359	a	119	c	146	g	409	t	168
25	5	IGIN						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
26	FEATURES	source						QY	1610	ACATGATGATGATGACTTAGCAGTGTCAAATCCTGTAGATAACGTCACAGTAGA	1669
27	2	QY						Db	1200	WYHWTATWWTATWATATAYMACPAWWWTATWAATWAWHTWAW	1141
28	3	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
29	4	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
30	5	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
31	6	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
32	7	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
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34	9	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
35	10	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
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37	12	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
38	13	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
39	14	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
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41	16	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
42	17	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
43	18	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
44	19	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
45	20	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
46	21	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
47	22	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
48	23	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
49	24	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
50	25	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
51	26	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
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53	28	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
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55	30	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
56	31	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
57	32	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
58	33	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
59	34	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
60	35	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
61	36	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
62	37	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
63	38	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
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65	40	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
66	41	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
67	42	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
68	43	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
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71	46	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
72	47	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
73	48	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
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75	50	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
76	51	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
77	52	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
78	53	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
79	54	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
80	55	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
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83	58	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
84	59	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
85	60	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
86	61	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
87	62	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
88	63	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
89	64	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
90	65	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
91	66	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
92	67	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
93	68	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
94	69	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
95	70	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
96	71	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
97	72	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
98	73	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
99	74	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
100	75	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
101	76	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
102	77	Db						QY	932	ATTPAAALAAWWTTPATTAACATTTWAAAAAATTTWAAATTAAT	1843
103	78	QY						Db	1844	ATTPAAALAAWWTTPATTAACATTTWAAAAAAT	

/mol_type="mRNA"
 /strain="17XL"
 /db_xref="taxon:73339"
 /clone="PVC070"
 /dev_stage="Asexual blood stages"
 /lab_host="E. coli XL-1 Blue"
 /clone_libr="PyBS"
 /note="Vector: PAD-GAL4: At 20-25% parasitemia, blood was collected from BALB/cByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose columns. Total RNA was isolated using the guanidinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XbaI and separated on a Sephadexyl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybrizAP arms directionally using EcoRI-XbaI cleaved arms. After packaging, the phagemid vector (PAD-GAL4) was excised from the HybrizAP vector and plasmid DNA.

BASE COUNT 424 a 23 c 131 g 109 t ORIGIN

Query Match 2.8%; Score 64.2; DB 12; Length 687; Best Local Similarity 49.5%; Pred. No. 0.23; Matches 165; Conservative 0; Mismatches 168; Indels 0; Gaps 0;

QY 1851 TGACAGCAACTAAAGATTCCTTTCATGAAATTAATAGCAAGAATGCT 1910
 Db 109 TGATGAGTAAATATGATGAGTAATAATGATGAGTGAAGTAAAGATAAAA 168

QY 1911 TTCTCAAACTGTTAACAGATAAACAAACTCGGATTAAAGATGTAANGAACCAT 1970
 Db 169 TGATGAGAAGAAAAAGACGAGAAGAAAAAGACGAGATAAAATGATGAGAAAGAA 228

QY 1971 TAATTTAAACATGGGAAAGTTAACACTTCAGGTTACCGAAGAGTTATCTTACCT 2030
 Db 229 AGACGAAAGTAAATATGATGAGTAAATAATGATGAGAAGAAAAAGACGAGTAAGAAA 288

QY 2031 TGCTAAAGAACAGATCTGAGGCATAAGTTAATAGCTTACGGCAAGAAGTAGCAA 2090
 Db 289 TGACGAGTAAACATGATGAGTAAATAATGATGAGTAAGAAAGACGAGTAAGAAA 348

QY 2091 TGCTACAGTTCAAAACAGGATAACAGAAGTGTGAGACACTGCTTTGAAATATAA 2150
 Db 349 TGATGAGTAAATAGATGAGTAAAGACGAGTAAACTGATGAGTAAAGAAA 408

QY 2151 AGAGGCCGTGTCTTCCACAGGGTTGATCAA 2183
 Db 409 TGACGAAAGTAAATGATGAGTAAAGATAAG 441

RESULT 7

BX415058 BX415058 1056 bp mRNA linear EST 15-MAY-2003

LOCUS BX415058 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP004YG19

DEFINITION 3'-PRIME: mRNA sequence.

ACCESSION BX415058

VERSION BX415058.1

EST. GI:30767520

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1056) Li, W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization. Unpublished Contact: Genoscope

FEATURES source

Location/Qualifiers 1. 1055

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0CAP004YG19"
 /tissue_type="THYMUS"
 /clone_libr="Homo sapiens THYMUS"
 /note="Vector: PCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched double strand cDNA was digested with Not I and cloned into the Not I and EcoRI sites of the PCMVSPORT 6 vector. Library was not normalized."

BASE COUNT 454 a 53 c 56 g 318 t ORIGIN

Query Match 2.8%; Score 64.2; DB 13; Length 1056; Best Local Similarity 33.9%; Pred. No. 0.23; Matches 186; Conservative 91; Mismatches 263; Indels 9; Gaps 1; Gaps 1;

QY 1694 ATTCTTATTTCGCGATAACATAATATGATCATCTTATTGAACTCAGTGGCATCCAG 1753
 Db 483 AAWTTTTTAWAWATTTWAAWAAWATTTWDKKKKKWTATAAAAAAAARAAAAA 542

QY 1754 AGAATTAGTTAGTGTATTTATGCTGAGTAAAGAGTTATACCTTAACCTATA 1813
 Db 543 AAAATATATATATATATATAKATAATAAWAAAAAATAATATAAAAAGAAWAT 602

QY 1814 ATTAAACATGAGAAACGGTGACTGGTTAGCTGGTACAGAGACTAAAGATTCCATT 1873
 Db 603 TTGWAAWATGTTTPTKTTWTTWATATTTWTTADATRKTPTTTWATDW 662

QY 1874 TGAATATGATTAATAATAATAGCAAGATGCTTCTCAAATGTAAACAGATA 1933
 Db 663 DATWAATATWTTWTRKGAGWAAAATAKTTKATAKTTKATAWAAAAGAAAAAAA 722

QY 1934 AACAAACACGCGAATTAAAGATGTTAACGACCAATTAAACATGGGAAGTT 1993
 Db 723 AAAAAGAAAAAAAWAAWTTTTTTWAAAGAAAATNNNNNTAWAWWWWWTTT 782

QY 1994 TAACCTTGAGGTTACCGAGGTATTCTTACCTTGCAAGAACAGATTCTGAAG 2053
 Db 783 TTTPTTTWWWWDDDDDTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 842

QY 2054 GCTATAAGGTAAAGTTAAGCTTATGCCAGAAGTGCAATGCTACAGTTCAAACAGGAA 2113
 Db 843 WWWWWWWWWAAAATAATTWTTWAWTTTATAAWWWWAATGTGTTWWAWAAA 902

QY 2114 TAACAAGTGTAGAGACACTTGCTTT-----GAAATATAAGACGCTGTGTC 2164
 Db 903 AAAAWTTAAWAAWAWTTWWAAWWTTKNAAAAAGAAAATTTT 962

QY 2165 CTACAGGAGGTGATCAAAGATCAATGGCTACTGTTAGTATCCCTGGTATCA 2224
 Db 963 TAGGAGGTTWAAAATAATGATWAATTATGTTTTWAAWDTATAATNTAGTA 1022

QY 2225 GTTGGGA 2233
 Db 1023 RTKKKKKKR 1031

RESULT 8

BX448176 BX448176 1169 bp mRNA linear EST 22-MAY-2003

LOCUS BX448176 Homo sapiens FETAL LIVER Homo sapiens cDNA clone

DEFINITION CS006YF18 3'-PRIME: mRNA sequence.

ACCESSION	BX448176
VERSION	BX448176.1
KEYWORD	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Mammalia: Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Li, W.B.; Gruber, C.; Jesse, J. and Polayes, D. Full-length cDNA libraries and normalization
REFERENCE	1 (bases 1 to 1169)
AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished
COMMENT	Contact: Genoscope
FEATURES	Genoscope - Centre National de Sequencing
source	BP 191 91006 ENR cedex - France
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1232.f. For more information about this cluster, see http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0AM006DC09NP&cluster=1232.f . Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0AM006DC09NP1.	
FEATURES	Location/Qualifiers
source	1. .1169
/organism="Homo sapiens"	
/mol_type="mRNA"	
/db_xref="taxon:9606"	
/clone="CS0AM006YF18"	
/tissue_type="FETAL LIVER"	
/dev_stage="fetal"	
/clone.lib="Homo sapiens FETAL LIVER"	
/note="Organ: liver; Vector: PCMSPORT-6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the PCMSPORT 6 vector. Library was not normalized."	
BASE COUNT	258
ORIGIN	a 127 c 167 g 437 t 180 others
Query Match	2.8%; Score 63.8; DB 13; Length 1169; Matches 222; Conservative 54; Mismatches 317; Indels 0; Gaps 0;
Oy	1615 AATGATAGTACTTTAGCAGTTGCTAAATCCTGTAGATAACCTCCTAAGATGATATCCT 1674
Db	845 AMGGACAKTTSYCATAAATGGATCTTMMCCWATCACCTCTCACCACATCATATAWAA 786
Oy	1675 CCACAGCTAACTGACCTGATCTTATTCGAATAACATAATATCACTCTTATT 1734
Db	785 ATATATAATTAACAGCTGCTTACATGCAAGAGTTAGTTGATATTATCTGTATGGAAAGATAAAAGAA 1794
Oy	1735 GGAACTCAGTGGCATCCAGAAGATTTAGTTGATATTATCTGTATGGAAAGATAAAAGAA 1794
Db	725 AAMAMAAATAATACAGACATAKTTTCAAGATCTT 666
Oy	1795 GTTATACCTGTACTCATTAATTAACATGAGAAACGGTACTGGTTAGCTGGAC 1854
Db	665 TRACTCTCATCAAGAGAACATAGAAATGTTGACWATCTRTCAAGCTTWGATGTGAC 606
Oy	1855 AGAACTAAAGATTCATTTGAAATGAAATAAATAATAGCAAGATGCTTCT 1914
Db	605 ACCTTATATGATTTCTCCAAWTTAACCTATATAAACACACAAAAAWAAA 546
Oy	1915 CAACAGTAAACAGATTAACAAACCTCGAATTAAAGATGTTAAGCAACCATAT 1974
Db	545 AAATATAAACAAAWATAAAACAAATCARRAAMACRAWATAATAMAWAGAAAAA 486
BASE COUNT	232
ORIGIN	a 19 c 80 g 64 t
Query Match	2.8%; Score 63.2; DB 12; Length 395; Matches 152; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

FEATURES		Location/Qualifiers	
Source			
		I. . 1044	
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		/mol-type="mRNA"	/lab_xref="taxon: 9605"
		/clone="C5C5CAP05YK01"	/tissue_type="THYMUS"
		/clone_id="Homo sapiens THYMUS"	/note="Vector: PCMVSPORT-6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned, into the Not I and EcoRV sites of the PCMVSPORT 6 vector. Library was not normalized."
BASE COUNT	123 a	130 c	89 g 513 t 189 others
ORIGIN			
Query Match		2.78; Score 61.6; DB 13; Length 1044; Matches 142; Conservative 35.3%; Pred. No. 0.67; Mismatches 176; Indels 4; Gaps 1;	
QY	1752	AGAGATTTAGTGTATTCGTTGAGATAAAAGAGTTATACCTGTAACCA 1811	
DB	987	AKKAKAAAKAAADAAADAAADKAAKKAKWDKADAAAKAAAKKKDKKAADKA 928	
QY	1812	TAATTACATTCGAGAAACCGTGTACTGGTTAGCTGTGACAGAACTTAAGATTC 1871	
DB	927	AAAAAACAAAADAAADKAAKKAKAAAKAAADAAWAAKKAKKAADAA 868	
QY	1872	TWTGAAATGAAATTAAGATAATAAGCAAGAATGTTCTCAACATGTAAACAGA 1931	
DB	867	AAKKAAKAAAKAAAKAAAKAAAKAAAKAAADAAAKKK----AAADDKAKAAAKKK 812	
QY	1932	TAACACAAACCTCGAATTAAAGATGSPAAACCACTTAATTAACATGGGAAAG 1991	
DB	811	KAAKAAAKAKKKAAAKAAAKKAKKAAAADKKWARKKAKAAAKKKAKKA 752	
QY	1992	TTCACATTCAGGTTCACAGAAGGTATTCTTACCTGTCAAAGAACAGATCTGA 2051	
DB	751	AAAAAKAKKWAKKKAAKKAKAAAKKAAKKWAADAKAKAKAAAKAKAA 692	
QY	2052	AGCTTATAGTTAAAGTTATAGCCAGAAGTAGCAATGCTACAGTTCAAAACGG 2111	
DB	691	AAADKKAKKAAKKAADKAAKKAADKAAKKAADKAADKAADKAADKA 632	
QY	2112	AAATACAGGTGTAGGAGACACTGCTTGTGAAATAATPAAGA 2153	
DB	631	AAKKAAKAAKAAKAAKAAAKAAAKAAWTATWAATAAAAKAA 590	
BASE COUNT	314 a	19 c	102 g 71 t
ORIGIN			
Query Match		2.78; Score 61.4; DB 12; Length 506; Best Local Similarity 50.2%; Pred. No. 0.71; Mismatches 151; Indels 0; Gaps 0;	
QY	1851	TGACAGAACTAAAGATTCATTTGAAATTGATAAAATAAGCAAGATGCT 1910	
DB	198	TGATGAACTAAAGATGATGAACTGAAATGATGAGAAGAAAKAGCAGAAGAAA 257	
QY	1911	TTCCTCAAACTGTAAACAGATAAAACAAACCUCGAATTAAAGATGCTAAGCAACAT 1970	
DB	258	AGACGAAGTAAAGATGATGAGAAGAAAAGAGCAAGACTAAAGATGATGAA 317	
QY	1971	TAATTAAACATGGGAAAGTTTACACTTCAGGTTACCGAAGGTATCTTACCT 2030	
DB	318	TGAGAAGAAAAAAAGAGCAACTAAAGATGAGAATGAGTAAAGATGAGTAA 377	
QY	2031	TGTCAGAAACAGATTCTGAGGCTATAAGTTAATGCCAAAGATGCA 2090	
DB	378	TGATGAGTAAAGAGCAAGAGAAATGATGAGTAAAGATGAGTAA 437	
QY	2091	TGCTCACAGTTCAAAACAGGATAACAGTGTAGACACTGTTGAAATATA 2150	
DB	438	TGATGAGTAAAGATGATGAGTAAAGATGAGTAAAGAGCAAGAGAA 497	
QY	2151	AGA 2153	
DB	498	AGA 500	
RESULT 14	-		
BM170012	BM170012	506 bp mRNA linear EST 04-DEC-2001	
LOCUS		EST572535 PyBS Plasmodium yoelii yoelii cDNA clone PYCP290 5', end, mRNA sequence.	
DEFINITION			
ACCESSION	BM170012		
KEYWORDS	EST.		
SOURCE			
ORGANISM			
REFERENCE	1 (bases 1 to 506)		
AUTHORS	Carlton, J.M., Daly, P.M., Long, C.A., Bergman, L.W., Vaidya, A.B.,		
JOURNAL	Plasmodium yoelii EST project at TIGR		
COMMENT	Unpublished		
TITLE	Contact: Jane Carlton		
PARASITE GENOMICS GROUP	Parasite Genomics Group		
THE INSTITUTE FOR GENOMIC RESEARCH	The Institute for Genomic Research		
9712 Medical Center Drive, Rockville, MD 20850, USA	9712 Medical Center Drive, Rockville, MD 20850, USA		
TEL: 301-530-9319	TEL: 301-530-9319		
FAX: 301-838-0208	FAX: 301-838-0208		
EMAIL: carlton@tigr.org	EMAIL: carlton@tigr.org		
For clone info, please contact the Malaria Research and Reference			
Reagent Resource Center, ATCC			
http://www.malaria.mr4.org/mr4pages/index.html			
Seq primer: ADF			
Location/Qualifiers			
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		/strain="1XL"	
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		/clone="PRCP290"	
		/dev_stage="Asexual blood stages"	
		/lab_host="E. coli XL-1 Blue"	
		/clone_id="PyBS"	
/note="Vector: PAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/cByJ mice infected with Py1XL parasites, and leukocytes removed by passage over microcrystalline cellulose columns. Total RNA was isolated using oligo(dT) cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and BcRT adaptors ligated to the blunt ends. The sample was cleaved with XbaI and separated on a Sephadex G-500 column. Size-fractionated cDNA was precipitated and ligated to HybrizAP arms directionally using EcoRI-XbaI cleaved arms. After packaging, the phagemid vector (PAD-GAL4) was excised from the HybrizAP vector and plasmid DNA isolated."			
Query Match		2.78; Score 61.4; DB 12; Length 506; Best Local Similarity 50.2%; Pred. No. 0.71; Mismatches 151; Indels 0; Gaps 0;	
QY	1851	TGACAGAACTAAAGATTCATTTGAAATTGATAAAATAAGCAAGATGCT 1910	
DB	198	TGATGAACTAAAGATGATGAACTGAAATGATGAGAAGAAAGAGCAGAAGAAA 257	
QY	1911	TTCCTCAAACTGTAAACAGATAAAACAAACCUCGAATTAAAGATGCTAAGCAACAT 1970	
DB	258	AGACGAAGTAAAGATGATGAGAAGAAAAGAGCAAGACTAAAGATGATGAA 317	
QY	1971	TAATTAAACATGGGAAAGTTTACACTTCAGGTTACCGAAGGTATCTTACCT 2030	
DB	318	TGAGAAGAAAAAAAGAGCAACTAAAGATGAGAATGAGTAAAGATGAGTAA 377	
QY	2031	TGTCAGAAACAGATTCTGAGGCTATAAGTTAATGCCAAAGATGCA 2090	
DB	378	TGATGAGTAAAGAGCAAGAGAAATGATGAGTAAAGATGAGTAA 437	
QY	2091	TGCTCACAGTTCAAAACAGGATAACAGTGTAGACACTGTTGAAATATA 2150	
DB	438	TGATGAGTAAAGATGATGAGTAAAGATGAGTAAAGAGCAAGAGAA 497	
QY	2151	AGA 2153	
DB	498	AGA 500	
RESULT 15	-		
BM169947	BM169947	770 bp mRNA linear EST 04-DEC-2001	
LOCUS		EST572470 PyBS Plasmodium yoelii yoelii cDNA clone PYCP202 5', end, mRNA sequence.	
DEFINITION			
ACCESSION	BM169947		
VERSION	BM169947.1		
KEYWORDS	EST.		
SOURCE	Plasmodium yoelii yoelii		
ORGANISM	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.		

AUTHORS Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W., Valdya, A.B., Fraser, C.M., and Carucci, D.J.
TITLE Plasmodium yoelii EST Project at TIGR

Search completed: August 19, 2003, 13:15:48
Job time : 4320 secs

FEATURES	Reagent Resource Center, ATCC http://www.malaria.mr4.org/mr4pages/index.html
source	Seq primer: ADF.
Location/Qualifiers	Location/Qualifiers
	1. . 770
	/organism="Plasmodium yoelii yoelii" /mol_type="mRNA" /strain="17XL" /db_xref="taxon:73239" /clone="PYCPZ02" /dev_stage="Asexual blood stages" /lab_host="E. coli XL-1 Blue" /clone_lib="PYBS" /note="Vector: PAD-GAL4: At 20-25% parasitemia, blood was collected from BALB/cByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose columns. Total RNA was isolated using the guanidinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XbaI and separated on a Sephadex 1 S-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XbaI cleaved arms. After packaging, the phagemid vector (PAD-GAL4) was excised from the HybriZAP vector and plasmid DNA isolated."
BASE COUNT	379 a 64 c 131 g 196 t
ORIGIN	Query Match 2.7%; Score 61.4; DB 12; Length 770; Best local Similarity 49.8%; Pred. No. 0.72; Mismatches 155; Conservative 0; Mismatches 156; Indels 0; Gaps 0
Matches	1 TTAGAAAAGAGAAGAAAAAAAGACGAAGTAAATGATGAGAAAAAAAGACGAA 60
Qy	1843 TTAGCTGGTCAGACTAAGATTCATTGTGAATTAAATAATAGCAA 190
Db	1 TTAGAAAAGAGAAGAAAAAAAGACGAAGTAAATGATGAGAAAAAAAGACGAA 60
Qy	1903 GAATTGCTTCTCAACTGTAAACAGATAAAACAAACCTCGATTAAGATGGTAA 196
Db	61 GTAAAAATGATGAGTAAAATGATGAGAAAAAAAGACGAGTAAATGAGCAA 126
Qy	1963 GCAACCATTAATTAACACATGGGAAGGTAAACACCTCGAAGTTACCGAGGTTAT 207
Db	121 GTAAAAATGATGAGTAAAATGATGAGTAAAAGACGAGTAAATGATGAA 180
Qy	2023 TCTTCTCTGTCAGAACAGATCTGAAGGCTATAAGTAAAGTTATGCCAGAA 206
Db	181 GTAAAAATGATGAGTAAAATGACGAAGTAAATGATGAGTAAAATGACGAA 240
Qy	2083 GTAGGAATGCTACAGTTCAAACAGGAAATACAACTGATGAGACACTTGCTTTGAA 214
Db	241 GTAAAACTGATGAGTAAAAGACGAAGTAAACTGATGAGTAAACTGATGAA 300
Qy	2143 AATATTAAGA 213
Db	301 GTAAAAACTGAA 311